

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH
AND HUMAN SERVICES
(B) STREET: BOX OTT
(C) CITY: BETHESDA
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 20892

(i) APPLICANT:

(A) NAME: PAVLAKIS, GEORGE N.
(B) STREET: 9 PURDUE COURT
(C) CITY: ROCKVILLE
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 20850

(i) APPLICANT:

(A) NAME: FELBER, BARBARA K.
(B) STREET: 9 PURDUE COURT
(C) CITY: ROCKVILLE
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 20850

(ii) TITLE OF INVENTION: METHOD OF ELIMINATING
INHIBITORY/INSTABILITY REGIONS OF mRNA

(iii) NUMBER OF SEQUENCES: 130

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORGAN & FINNEGAN
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: 02-MAY-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/050,478
(B) FILING DATE: 26-OCT-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US93/02908
(B) FILING DATE: 29-MAR-1993
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/858,747
(B) FILING DATE: 27-MAR-1992
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MARRY, MARY J.

(B) REGISTRATION NUMBER: 34,398
(C) REFERENCE/DOCKET NUMBER: 2026-4006US1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212)758-4800
(B) TELEFAX: (212)751-6849

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 1:

ATGGGTGCGA GAGCGTCA GT ATTAAAGCGGG GGAGAATTAG ATCGATGGGA AAAAATTCCG	60
TTAAGGCCAG GGGGAAAGAA AAAATATAAA TAAACATA TAGTATGGC AAGCAGGGAG	120
CTAGAACGAT TCGCAGTTAA TCCTGCCCTG TTAGAACAT CAGAAGGCTG TAGACAAATA	180
CTGGGACAGC TACAACCATC CCTTCAGACA GGATCAGAAG AACTTAGATC ATTATATAAT	240
ACAGTAGCAA CCCTCTATTG TGTGCATCAA AGGATAGAGA TAAAAGACAC CAAGGAAGCT	300
TTAGACAAAGA TAGAGGAAGA GCAAAACAAA AGTAAGAAA AAGCACAGCA AGCAGCAGCT	360
GACACAGGAC ACAGCAATCA GGTCAGCCAA ATTAC	396

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 2:

CCAGGGGGAA AGAAAAAATA TAAATAAAAA CATATAGTAT GGGCAAGCAG G	51
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(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 3:

CCTTCAGACA GGATCAGAAG AACTTAGATC ATTATATAAT ACAGTAGC	48
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(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTIONS:SEQ ID NO: 4:

ACCCCTCTATT GTGTGCATCA AAGGATAGAG ATAAAAGACA CCAAGGAAGC	50
---	----

(6) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GAGCAAAACA AAAGTAAGAA AAAAGCACAG CAAGCAGCAG CTGACACAGG

50

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCAGGGGAA AGAAGAAAGTA CAAGCTAAAG CACATCGTAT GGGCAAGCAG G

51

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCTTCAGACA GGATCAGAGG AGCTTCGATC ACTATACAAC ACAGTAGC

48

(9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACCCCTCTATT GTGTGCACCA GCGGATCGAG ATCAAGGACA CCAAGGAAGC

50

(10) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GAGCAAAACA AGTCCAAGAA GAAGGCCAG CAGGCAGCAG CTGACACAGG

50

(11) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GAATAGTGCT GTTAACCTCC TGAACGCTAC CGCTATGCC GTGGCGGAAG GAACCGACAG

60

GGTTATAG

68

(12) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AAGTATTACA AGCCGCCATAC CGCGCCATCA GACATATCCC CGGCCGCATC CGCCAGGGCT

60

TG

62

(13) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GCTATAAGAT GGGCGGTAAA TGGAGCAAGT CCTCCGTAT CGGCTGGCCT GCTGTAAG

58

(14) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGAAAGAATG CGCAGGGCCG AACCCGCCGC CGACGGAGTT GGCGCCGTAT CTCGAGAC

58

(15) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTAGAAAAAC ACGCGCCAT TACCTCCTCT AACACGCCG CCAATAACGC CGCTTGTGCC

60

TG

62

(16) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
GCTAGAAGCA CAGGAAGAAG AGGAAGTCGG CTTCCCCGTT ACCCCTCAGG TACCTTAAG 60

(17) INFORMATION FOR SEQ ID NO: 16:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
TGAAAACGTT CGCATGTGTC GCTACGTTGC TTACTAAGAT GGA 43

(18) INFORMATION FOR SEQ ID NO: 17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
TTCTCAGATA CCTAGCTTC AATTGCCCTA TTGTCTACCT TGA 43

(19) INFORMATION FOR SEQ ID NO: 18:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
GCCCTGTGAG TAGGCAGTGA AGGACAGCCA TACGTAACAT ACAAGTGCCA 50

(20) INFORMATION FOR SEQ ID NO: 19:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
AGCAGCAGCA ATGAACCTAG TAGCGATAGC CTGAGTAGCC CTACGCTGCT G 51

(21) INFORMATION FOR SEQ ID NO: 20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
ACCCCGAGGC AGATAGCTT CCATCCTGCG CTGCCGCTCA CCGCAAGGGC 50

(22) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CTGCACAGTG GAAGCCTCGG AATGGGCCCT ATGGCTACCG AATTGGAACC ACTGTGCACT C

61

(23) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CACCTAGAAC TTTAAATGCA TGGGTAAAAG TAGTAGAAGA GAAGGCT

47

(24) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CACCTAGAAC CCTGAACGCC TGGGTGAAGG TGGTAGAAGA GAAGGCT

47

(25) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCACCCCAACA AGATTAAAC ACCATGCTAA ACACAGTGGG GGGAC

45

(26) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCACCCCAACA GGACCTGAAC ACGATGTTGA ACACCGTGGG GGGAC

45

(27) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CAGTAGGAGA AATTATAAA AGATGGATAA TCCTG

35

(28) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CAGTAGGAGA GATCTACAAG AGGTGGATAA TCCTG

35

(29) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGATTAATAA AAATAGTAAG AATGTATAGC CCTACC

36

(30) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGATTGAACA AGATCGTGAG GATGTATAGC CCTACC

36

(31) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

ACCGGTTCTA TAAAATCTA AGAGCCGAGC AAGCTTCACA G

41

(32) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ACCGGTTCTA CAAGACCCCTG CGGGCTGAGC AAGCTTCACA G

41

(33) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATTGTAAGAC TATTTAAAAA GCATGGGAC CAGCGGCTAC ACTA

44

(34) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATTGTAAGAC CATCCTGAAG GCTCTCGGCC CAGCGGCTAC ACTA

44

(35) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AGAGTTTG GCTGAAGCAAT GAGCCAAGTA ACAAATTCA GCTACCAATAAT G

51

(36) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

AGAGTTTG GCGAGGCGAT GAGCCAGGTG ACGAACTCGG CGACCATAAT G

51

(37) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CAGAGAGGCA ATTTAGGAA CCAAAGAAAG ATTGTTAAGT GTTCAATTG T

51

(38) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 BASE PAIRS
(B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CAGAGAGGCA ACTTCCGGAA CCAGCGGAAG ATCGTCAAGT GTTCAATTG T

51

(39) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GAAGGGCACA CAGCCAGAAA TTGCAGGGCC CCTAGGAAAA AGGGCTGT

48

(40) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GAAGGGCACA CCGCCAGGAA CTGCCGGGCC CCCCGGAAGA AGGGCTGT

48

(41) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TGTGGAAAGG AAGGACACCA AATGAAAGAT TGTACTGAGA GACAGGCTAA T

51

(42) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

TGTGGAAAGG AGGGGCACCA GATGAAGGAC TGCACGGAGC GGCAGGGCTAA T

51

(43) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CCCCCTCGTCA CAATAAAGAT AGGGGGCAA CTAAAGGAAG CTCTATTAGA TACAGGAG

58

(44) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCCCCTCGTCA CAGTAAGGAT CGGGGGGCAA CTCAGGAAG CGCTGCTCGA TACAGGAG

58

(45) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GATAGGGGGA ATTGGAGGTT TTATCAAAGT AAGACAGTAT GATCAGATAC TC

52

(46) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GATAGGGGGG ATCGGGGGCT TCATCAAAGT GAGGCAGTAC GACCAGATAC TC

52

(47) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CCTATTGAGA CTGTACCACT AAAATTAAG CCAGGAATGG ATGGCCCA

48

(48) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTATTGAGA CGGTGCCCGT GAAGTTGAAG CCGGGGATGG ATGGCCCA

48

(49) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 BASE PAIRS

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

CAATGGCCAT TGACAGAAGA AAAAATAAAA GCATTAGTAG AAATTTGTAC AGAGA

55

(50) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAATGGCCAT TGACGGAAGA GAAGATCAAG GCCTTAGTCG AAATCTGTAC AGAGA

55

(51) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TTCAGGAAGT ATACTGCATT TACCATACCT AGTATAAAC A ATGAGACACC A

51

(52) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCAGGAAGT ACACGGCGTT CACCATCCCCG AGCATCAACA ACGAGACACC A

51

(53) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TTAGTGGGGA AATTGAATTG GGCAAGTCAG ATTTACCCAG GGATTAAG

49

(54) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 49 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TTAGTGGGGA AGGTGAAC TG GGCGAGCCAG ATCTACCCGG GGATTAAG

49

(55) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GGCCAATGGA CATAATCAAAT TTATCAAGAG CCATTTAAA ATCTGAAAAC AGG

53

(56) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GGCCAATGGA CGTACCAAGAT CTACCAAGGAG CCGTTCAAGA ACCTGAAAAC AGG

53

(57) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGGGGAAAGA CTCCTAAATT TAAACTGCC ATACAAAAGG AAACATGGG

49

(58) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGGGGAAAGA CGCCGAAGTT CAAGCTGCC ATCCAGAAGG AGACATGGG

49

(59) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GAAGACTGAG TTACAAGCAA TTTATCTAGC TTTGCAGGAT TCGGGATTAG

50

(60) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GAAGACTGAG CTGCAGGCAGA TCTACCTGGC GCTGCAGGAC TCGGGATTAG

50

(61) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GTTAGTCAAT CAAATAATAG AGCAGTTAAT AAAAAAGGAA AAGGTCTATC TGGCAT

56

(62) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GTTAGTCAAC CAAATCATCG AGCAGCTGAT CAAGAAGGAG AAGGTGTATC TGGCAT

56

(63) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GTCAGTGCTG GAATCAGGAA AGTACTATTT TTAGATGGAA TAGATAAGGC CC

52

(64) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GTCAGTGCTG GGATCCGGAA GGTGCTATTC CTGGACGGGA TCGATAAGGC CC

52

(65) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAACATGAGA AATATCACAG TAATTGGAGA GCAATGGCTA GTGATTTAA CCTGCCAC

58

(66) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GAACATGAGA AGTACCACTC CAACTGGCGC GCTATGGCCA GCGACTTCAA CCTGCCAC

58

(67) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GGAATATGGC AACTAGATTG TACACATTTA GAAGGAAAAG TTATCCTGGT AG

52

(68) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GGAATATGGC AGCTGGACTG CACGCACCTG GAGGGGAAGG TGATCCTGGT AG

52

(69) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GCAGAAGTTA TTCCAGCAGA AACAGGGCAG GAAACAGCAT ATTTCTTTT AAAATTAGCA

60

GGAAGA

66

(70) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GCAGAAGTTA TCCCTGCTGA AACTCGGCAG GAGACGGCCT ACTTCCTGCT CAAACTCGCA

60

GGAAGA

66

(71) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGGCCAGTAA AAACAATACA TACTGACAAT GGCAGCAATT TCACCGGTGC TACGG

55

(72) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TGGCCAGTGA AGACGATCCA CACGGACAAC GGAAGCAACT TCACTGGTGC TACGG

55

(73) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GGAGTAGTAG AATCTATGAA TAAAGAATTA AAGAAAATTA TAGGACAGGT AA

52

(74) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GGAGTAGTAG AATCCATGAA CAAGGAACTG AAGAAGATCA TCGGACAGGT AA

52

(75) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TGGCCAGTAA AAACAATACA CACGGACAAC GGAAGCAACT TCACTGGTGC TACGG

55

(76) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CTTGGGATGT TGATGATCTG TAGTGCTACA GAAAATTGT GGGTC

45

(77) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CTTGGGATGC TGATGATCTG CAGGCCACC GAGAAGCTGT GGGTC

45

(78) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATTATGGGT ACCTGTGTGG AAG

23

(79) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

ATTATGGCGT GCCCGTGTGG AAG

23

(80) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CACTCTATTT TGTGCACTAG ATGCTAAAGC ATATGAT

37

(81) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CACTCTATTC TGGCCCTCCG ACGCCAAGGC ATATGAT

37

(82) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACAGAGGTAC ATAATGTTG GGCCAC

26

(83) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

ACAGAGGTGC ACAACGTCTG GGCCAC

26

(84) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CCAACCCACA AGAAGTAGTA TTGGTAAATG TGACAGAAAA TTTAACATG TG

52

(85) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCAACCCCCA GGAGGTTGGTG CTGGTGAACG TGACCGAGAA CTTAACATG TG

52

(86) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TAACCCCCACT CTGTGTTAGT TTAAAGTGCA CTGATTTGAA GAATG

45

(87) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TAACCCCCCT CTGGGTGAGC CTGAAGTGCA CCGACCTGAA GAATG

45

(88) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

ATCAGCACAA GCATAAGAGG TAAGGTGCAG

30

(89) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

ATCAGCACCA GCATCCGCGG CAAGGTGCAG

30

(90) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GAATATGCAT TTTTTATAA ACTTGATATA ATA

33

(91) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

GAATATGCCT TCTTCTACAA GCTGGATATA ATA

33

(92) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CCAATAGATA ATGATACTAC CAGCTAT

27

(93) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCAATAGCTA AGGACACCA CAGCTAT

27

(94) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GCCCCGGCTG GTTTGCGAT TCTAAAATGT AATAATAAGA CGTTC

45

(95) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GCCCCGGCCG GCTTCGCGAT CCTGAAGTGC AACACAACAAGA CGTTC

45

(96) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CAACTGCTGT TAAATGGCAG TCTAGCAGAA GAAGAGGTAG TA

42

(97) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CAACTGCTGC TGAACGGCAG CCTGGCCAG GAGGAGGTAG TA

42

(98) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCTGTCAATT TCACGGACAA TGCTAAAACC ATAAT

35

(99) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TCTGCCAACT TCACCGACAA CGCCAAGACC ATAAT

35

(100) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTGAACACAT CTGTAGAAAT TAATTGTACA AG

32

(101) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CTGAACCAGT CCGTGGAGAT CAACTGTACA AG

32

(102) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CAACAACAAT ACAAGAAAAA GAATCCGTAT C

31

(103) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CAACAACAAAC ACCGGCAAGC GCATCCGTAT C

31

(104) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

GCTAGCAAAT TAAGAGAAC AATTTGGAAAT AATAAAACAA TAATCTT

47

(105) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GCTAGCAAGC TGCAGGAGCA GTACGGGAAC AACAAAGACCA TAATCTT

47

(106) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

TTCTACTGTA ATTCAACACA ACTGTTAAC AGTACTTGGT TTAAT

45

(107) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

TTCTACTGGA ACTCCACCCA GCTGTTAAC AGCACCTGGT TTAAT

45

(108) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CACAATCACC CTCCCATGCA GAATAAAACA AATTATAAAC ATG

43

(109) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CACAATCACC CTGCCCTGCC GCATCAAGCA GATCATAAAC ATG

43

(110) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCAGTGGAA CAAATTAGAT GTTCATCAAA TATTACAGGG CTGCTA

46

(111) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

CATCAGCGGC CAGATCCGCT GCTCCTCCAA CATCACCGGG CTGCTA

46

(112) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

GAGGGACAAT TGGAGAAGTG AATTATATAA ATATAAAGTA GTAAAAATTG AACCATTA

58

(113) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GAGGGACAAC TGGAGGAGCG AGCTGTACAA GTACAAGGTG GTGAAGATCG AACCATTA

58

(114) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:
GCCTTGAAT GCTAGTTGGA GTAATAAATC TCTGGAACAG 40

(115) INFORMATION FOR SEQ ID NO: 114:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:
GCCTTGAAC GCCAGCTGGA GCAACAAGTC CCTGGAACAG 40

(116) INFORMATION FOR SEQ ID NO: 115:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:
GAGTGGGACA GAGAAATTAA CAATTACACA AG 32

(117) INFORMATION FOR SEQ ID NO: 116:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:
GAGTGGGACC GCGAGATCAA CAACTACACA AG 32

(118) INFORMATION FOR SEQ ID NO: 117:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:
ATACACTCCT TAATTGAAGA ATCGCAAAAC CAGCAAGAAA AGAATGAA 48

(119) INFORMATION FOR SEQ ID NO: 118:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:
ATACACTCCC TGATCGAGGA GTCCCAGAAC CAGCAGGAGA AGAATGAA 48

(120) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CAGGCCGAA GGAATAGAAG AAGAAGGTGG AGAGAGAGAC

40

(121) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CAGGCCGAG GGCATCGAGG AGGAGGGCGG CGAGAGAGAC

40

(122) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

TACCACCGCT TGAGAGACTT ACTCTTGATT GTAACGAGGA TTGTGGAACT

50

(123) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TACCACCGCC TGCACGACCT GCTCCTGATC GTGACGAGGA TCGTGGAACT

50

(124) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

GGTGGGAAGC CCTCAAATAT TGGTGGAAATC TCCTACAGTA TTGG

44

(125) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GGTGGGAGGC CCTCAAGTAC TGGTGAACC TCCTCCAGTA TTGG

44

(126) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

AGTCAGGAAC TAAAGAATAG TGCTGTTAGC TTGCTCAATG

40

(127) INFORMATION FOR SEQ ID NO: 126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

AGTCAGGAGC TGAAGAACAG CGCCGTGAAC CTGCTCAATG

40

(128) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GGTACCAAGCA CACAAAGGAA TTGGAGGAAA TGAACAAGTA GATAAATTAG TCAGTGCTGG
AATCAGGAAA GTACTATTT TAGATGGAAT AGATAAGGCC CAAGATGAAC ATGAGAAATA
TCACAGTAAT TGGAGAGCAA TGGCTAGTGA TTTAACCTG CCACCTGTAG TAGCAAAGA
AATAGTAGGCC AGCTGTGATA AATGTCAGCT AAAAGGAGAA GCCATGCATG GACAAGTAGA
CTGTAGTCCA GGAATATGGC AACTAGATTG TACACATTGAAAGGAAAAG TTATCCTGGT
AGCAGTTCAT GTAGCCAGTG GATATATAGA AGCAGAAGTT ATTCAGCAG AAACAGGGCA
GGAAACAGCA TATTTCTTT TAAAATTAGC AGGAAGATGG CCAGTAAAAA CAATACATAC
TGACAAATGGC AGCAATTCA CCGGTGCTAC GGTTAGGGCC GCCTGTTGGT GGGCGGGAAAT
CAAGCAGGAA TTTGG

60

120

180

240

300

360

420

480

495

(129) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7228 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

TGGAAGGGCT AATTGGTCC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA	60
CACAAGGGCTA CTTCCCTGAT TGGCAGAAGT ACACACCAGG GCCAGGGATC AGATATCCAC	120
TGACCTTGG ATGGTGCTTC AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA	180
AATAAGGAGA GAAGAACAGC TTGTTACACC CTATGAGCCA GCATGGGATG GAGGACCCGG	240
AGGGAGAAAGT ATTAGTGTTG AAGTTTGACA GCCTCCTAGC ATTCGTCAC ATGGCCCGAG	300
AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG GGACTTCCG	360
CTGGGGACTT TCCAGGGAGG TGTGGCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT	420
GCTACATATA AGCAGCTGCT TTTTGCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA	480
GCCTGGGAGC TCTCTGGCTA ACTAGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCT	540
TGAGTGCTCA AAGTAGTGTG TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC	600
AGACCCCTTT AGTCAGTGTG GAAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAAG	660
CGAAAGTAAA GCCAGAGGGAG ATCTCTCGAC GCAGGACTCG GCTTGCTGAA GCGCGCGTCG	720
ACAGAGAGAT GGGTGCAGA GCGTCAGTAT TAAGGGGGGG AGAATTAGAT CGATGGGAAA	780
AAATTGGTT AAGGCCAGGG GGAAAGAAGA AGTACAAGCT AAAGCACATC GTATGGCAA	840
GCAGGGAGCT AGAACGATTC GCAGTTAATC CTGGGCTGTT AGAAACATCA GAAGGCTGTA	900
GACAAATACT GGGACAGCTA CAACCATCCC TTCAGACAGG ATCAGAGGGAG CTTCGATCAC	960
TATACAACAC AGTAGCAACC CTCTATTGTG TGCAACCGAGG GATCGAGATC AAGGACACCA	1020
AGGAAGCTT AGACAAGATA GAGGAAGAGC AAAACAAGTC CAAGAAGAAG GCCCAGCAGG	1080
CAGCAGCTGA CACAGGACAC AGCAATCAGG TCAGCCAAA TTACCCCTATA GTGCAGAACAA	1140
TCCAGGGGCA AATGGTACAT CAGGCCATAT CACCTAGAAC TTTAAATGCA TGGGTAAAAG	1200
TAGTAGAAGA GAAGGCTTTC AGCCCAGAAG TGATAACCAT GTTTCAGCA TTATCAGAAG	1260
GAGCCACCCC ACAGGACCTG AACACGATGT TGAACACCGT GGGGGGACAT CAAGCAGCCA	1320
TGCAAATGTT AAAAGAGACC ATCAATGAGG AAGCTGCAGA ATGGGATAGA GTGCATCCAG	1380
TGCATGCAGG GCCTATTGCA CCAGGCCAGA TGAGAGAAC AAGGGGAAGT GACATAGCAG	1440
GAACCTACTAG TACCCCTTCAG GAACAATAG GATGGATGAC AAATAATCCA CCTATCCCG	1500
TAGGAGAGAT CTACAAGAGG TGGATAATCC TGGGATTGAA CAAGATCGTG AGGATGTATA	1560
GCCCTTACCAAG CATTCTGGAC ATAAGACAAG GACCAAAGGA ACCCTTTAGA GACTATGTAG	1620
ACCGGTTCTA TAAAACCTCA AGAGCTGAGC AAGCTTCACA GGAGGTAAAA AATTGGATGA	1680
CAGAAACCTT GTTGGTCAA AATGCGAACCC CAGATTGTAAC GACCATCCTG AAGGCTCTCG	1740
GCCCAGCGGC TACACTAGAA GAAATGATGA CAGCATGTCA GGGAGTAGGA GGACCCGGCC	1800
ATAAGGCAAG AGTTTGATG GGATCCACTA GTTCTAGACT CGAGGGGGGG CCCGGTACCT	1860
TTAAGACCAA TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTAAA AGAAAAGGGG	1920
GGACTGGAAG GGCTAATTCA CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC	1980
CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAAGATAT	2040
CCACTGACCT TTGGATGGTG CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAGAAGAG	2100
GCCAATAAAG GAGAGAACAC CAGCTTGTTA CACCCGTGTA GCCTGCATGG AATGGATGAC	2160

CCTGAGAGAG AAGTGTAGA GTGGAGGTTT GACAGCCGCC TAGCATTCA TCACGTGGCC	2220
CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC GAGCTTGCTA CAAGGGACTT	2280
TCCGCTGGGG ACTTTCCAGG GAGGCGTGGC CTGGGCGGGG CTGGGGAGTG GCGAGCCCTC	2340
AGATGCTGCA TATAAGCAGC TGCTTTTGCT CTGTAAGTGGG TCTCTCTGGT TAGACCAGAT	2400
CTGAGCCTGG GAGCTCTG GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT	2460
GCCTTGAGTG CTTCAAGTAG TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC	2520
CCTCAGACCC TTTTAGTCAG TGTGGAAAAT CTCTAGCACC CCCCAGGAGG TAGAGGTTGC	2580
AGTGAGCCAA GATCGCGCCA CTGCATTCCA GCCTGGCAA GAAAACAAGA CTGTCTAAAA	2640
TAATAATAAT AAGTTAAGGG TATTAATAT ATTATACAT GGAGGTATA AAAATATATA	2700
TATTTGGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTTGGGAGG CCGAGGCAGG	2760
TGGATCACCT GAGTTTGGGA GTTCCAGACCC AGCCTGACCA ACATGGAGAA ACCCCTCTC	2820
TGTGTATTT TAGTAGATTT TATTTATGT GTATTTATT CACAGGTATT TCTGGAAAAC	2880
TGAAACTGTT TTTCCCTCTAC TCTGATACCA CAAGAATCAT CAGCACAGAG GAAGACTCT	2940
GTGATCAAAT GTGGTGGGAG AGGGAGGTTT TCACCCAGCAC ATGAGCAGTC AGTTCTGCCG	3000
CAGACTCGGGC GGGTGTCCCT CGGTTAGTT CCAACACCGC CTGCCTGGAG AGAGGTCAGA	3060
CCACAGGGTG AGGGCTCACT CCCCAAGACA TAAACACCCA AGACATAAAC ACCCAACAGG	3120
TCCACCCCGC CTGCTGCCCA GGCAGAGCCG ATTCAACCAAG ACGGGAATTA GGATAGAGAA	3180
AGAGTAAGTC ACACAGAGCC GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAATCA	3240
GTCTCCCCAA GCATTGGGG ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG	3300
TGAGTTGGAG ATGAAAGCGT AGGGAGTCGA AGGGTGTCCCT TTGCGCCGAG TCAGTTCTG	3360
GGTGGGGGCC ACAAGATCGG ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT	3420
GGAGTGCAGG GTCTGCAAA TATCTCAAGC ACTGATTGAT CTTAGGTTT ACAATAGTGA	3480
TGTTACCCCA GGAACAATTG GGGGAAGGTC AGAATCTGT AGCCTGTAGC TGCATGACTC	3540
CTAAACCATA ATTTCTTTT TGTTTTTTT TTTTATTT TGAGACAGGG TCTCACTCTG	3600
TCACCTAGGC TGGAGTGCAG TGGTGCAATC ACAGCTCACT GCAGCCCTA GAGCGGGCCG	3660
CACCCGGGTG GAGCTCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTG	3720
TTTTACAAGC TCGTGAATGGG GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC	3780
ATCCCCCTTT CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC	3840
AGTTGGCGAG CCTGAATGGC GAATGGCCCG AAATTGTAAA CGTTAATATT TTGTTAAAT	3900
TCGGCTTAAA TTTTGTAA ATCAGCTCAT TTTTAACCA ATAGGCCAA ATCGGCAAAA	3960
TCCCTTATAA ATCAAAGAA TAGACCGAGA TAGGGTTGAG TGTTGTTCCA GTTGGAAACA	4020
AGAGTCCACT ATAAAGAAC GTGGACTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG	4080
GCGATGGCCC ACTACGTGAA CCATCACCCCT AATCAAGTTT TTTGGGTGCG AGGTGCCGTA	4140
AAGCACTAAA TCGGAACCCCT AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG	4200
CGAACGTGGC GAGAAAGGAA GGGAAAGAAAG CGAAAGGGAGC GGGCGCTAGG GCGCTGGCAA	4260

GTGTAGCGGT CACGCTGGC GTAACCACCA CACCCGCCGC GCTTAATGCG CGCCTACAGG	4320
GGCGCGTCCA GGTGGCACCT TTGGGGAAA TGTCGGCGGA ACCCCTATTT GTTATTTTT	4380
CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCATA	4440
ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTA TTCCCTTTT	4500
TGCGGCATTT TGCCCTCCG TTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAGATGC	4560
TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT	4620
CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTA AAGTTCTGCT	4680
ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACA	4740
CTATTCTAG AATGACTTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG	4800
CATGACAGTA AGAGAATTAT GCACTGCTGC CATAACCATG AGTGATAACA CTGCGGCCAA	4860
CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTGC ACAACATGGG	4920
GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA	4980
CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAAACG TTGGCCAAAC TATTAACTGG	5040
CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAAGT	5100
TGCAGGGACCA CTTCTGCCCT CGGCCCTTC CGCTGGCTGG TTTATTGCTG ATAAATCTGG	5160
AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC	5220
CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA	5280
GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAAGACC AAGTTTACTC	5340
ATATATACTT TAGATTGATT TAAAACCTCA TTTTTAATT AAAAGGATCT AGGTGAAGAT	5400
CCTTTTGAT AATCTCATGA CAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC	5460
AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTTCTGC GCGTAATCTG	5520
CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT TGGTGGCCGG ATCAAGAGCT	5580
ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCT	5640
TCTAGTGTAG CGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT	5700
CGCTCTGCTA ATCCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG	5760
GTTGGACTCA AGACGATACT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTT	5820
GTGCACACAG CCCAGCTTG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA	5880
GCTATGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG	5940
CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCAGGG GGAAACGCCCT GGTATCTTA	6000
TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GTCGTCA	6060
GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCCTT TTACGGTTCC TGGCCTTTG	6120
CTGGCCTTT GCTCACATGT TCTTCTGCTC GTTATCCCCCT GATTCTGTGG ATAACCGTAT	6180
TACCGCCTT GAGTGAAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC	6240
AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC	6300
GATTCACTAA TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA	6360
CGCAATTAAT GTGAGTTAGC TCACTCACTA GGCACCCCAAG GCTTACACT TTATGCTTCC	6420

GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATT CACACAGGAA ACAGCTATGA	6480
CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC TGCTGCAGGG	6540
TCCCTAACTG CCAAGCCCCA CAGTGTGCC TGAGGCTGCC CCTTCCTTCT AGCGGGCTGCC	6600
CCCACTCGGC TTTGCTTCC CTAGTTCAAG TTACTTGCGT TCAGCCAAGG TCTGAACTA	6660
GGTGCACACA GAGCGGTAAG ACTGCAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA	6720
CACTGCACCC TGACAGTCGT CAGCCTCACA GGGGGTTTAT CACATTGCAC CCTGACAGTC	6780
GTCAAGCTCA CAGGGGGTTT ATCACAGTGC ACCCTTACAA TCATTCCATT TGATTCACAA	6840
TTTTTTAGT CTCTACTGTG CCTAACTTGT AAGTTAAATT TGATCAGAGG TGTGTTCCCA	6900
GAGGGGAAAA CAGTATATAC AGGGTTCACT ACTATCGCAT TTCAAGGCCTC CACCTGGTC	6960
TTGGAATGTG TCCCCCGAGG GGTGATGACT ACCTCAGTTG GATCTCCACA GGTCAACAGTG	7020
ACACAAGATA ACCAAGACAC CTCCCAAGGC TACCAAAATG GGCCGCCCTC CACGTGCACA	7080
TGGCCGGAGG AACTGCCATG TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCCTGGTG	7140
TGGAGGGAGG GACCAGCGCA GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG	7200
CCCCAGTTCT ACTTACACCA GGAAAGGC	7228

(130) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7228 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGGAAGGGCT AATTGGTCC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA	60
CACAAGGCTA CTTCCCTGAT TGGCAGAACT ACACACCCAGG GCCAGGGATC AGATATCCAC	120
TGACCTTGG ATGGTGCTTC AAGTTAGTAC CAGTTAACCC AGAGCAAGTA GAAGAGGCCA	180
ATAAGGAGA GAAGAACAGC TTGTTACACC CTATGAGCCA GCATGGGATG GAGGACCCGG	240
AGGGAGAACT ATTAGTGTGG AAGTTTACA GCCTCCTAGC ATTCGTCAC ATGGCCCGAG	300
AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG GGACTTTCCG	360
CTGGGACTT TCCAGGGAGG TGTGGCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT	420
GCTACATATA AGCAGCTGCT TTTGCTCTG ACTGGGTCTC TCTGGTTAGA CCAGATCTGA	480
GCCTGGGAGC TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCT	540
TGAGTGTCA AAGTAGTGTG TGCCCGCTG TTGTGTGACT CTGGTAACCA GAGATCCCTC	600
AGACCCCTTT AGTCAGTGTG GAAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAAG	660
CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG GCTTGCTGAA GCCCGCGTCG	720
ACAGAGAG ATG GGT GCG AGA GCG TCA GTA TTA AGC GGG GGA GAA TTA GAT	770
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp	
1 5 10	
CGA TGG GAA AAA ATT CGG TTA AGG CCA GGG GGA AAG AAG AAG TAC AAG	818
Arg Trp Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys	
15 20 25 30	

CTA AAG CAC ATC GTA TGG GCA AGC AGG CTA GAA CGA TTC GCA GTT Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val 35 40 45	866
AAT CCT GGC CTG TTA GAA ACA TCA GAA GGC TGT AGA CAA ATA CTG GGA Asn Pro Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly 50 55 60	914
CAG CTA CAA CCA TCC CTT CAG ACA GGA TCA GAG GAG CTT CGA TCA CTA Gln Leu Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu 65 70 75	962
TAC AAC ACA GTA GCA ACC CTC TAT TGT GTG CAC CAG CGG ATC GAG ATC Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile 80 85 90	1010
AAG GAC ACC AAG GAA GCT TTA GAC AAG ATA GAG GAA GAG CAA AAC AAG Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Gln Asn Lys 95 100 105 110	1058
TCC AAG AAG AAG GCC CAG GCA GCA GCT GAC ACA GGA CAC AGC AAT Ser Lys Lys Lys Ala Gln Gln Ala Ala Asp Thr Gly His Ser Asn 111 115 120 125	1106
CAG GTC AGC CAA AAT TAC CCT ATA GTG CAG AAC ATC CAG GGG CAA ATG Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met 130 135 140	1154
GTA CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA AAA GTA Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val 145 150 155	1202
GTA GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT TCA GCA Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala 160 165 170	1250
TTA TCA GAA GGA GCC ACC CCA CAG GAC CTG AAC ACG ATG TTG AAC ACC Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr 175 180 185 190	1298
GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC ATC AAT Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn 195 200 205	1346
GAG GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA GGG CCT Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro 210 215 220	1394
ATT GCA CCA CGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA GCA GGA Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly 225 230 235	1442
ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT AAT CCA Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro 240 245 250	1490
CCT ATC CCA GTA GGA GAG ATC TAC AAG AGG TGG ATA ATC CTG GGA TTG Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu 255 260 265 270	1538
AAC AAG ATC GTG AGG ATG TAT AGC CCT ACC AGC ATT CTG GAC ATA AGA Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg 275 280 285	1586
CAA GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC TAT AAA Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys 290 295 300	1634
ACT CTA AGA GCT GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG ATG ACA	1682

Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr			
305	310	315	
GAA ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACC ATC CTG			1730
Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu			
320	325	330	
AAG GCT CTC GGC CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA GCA TGT			1778
Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys			
335	340	345	350
CAG GGA GTA GGA GGA CCC GGC CAT AAG GCA AGA GTT TTG TAG			1820
Gln Gly Val Gly Pro Gly His Lys Ala Arg Val Leu			
355	360		
GGATCCACTA GTTCTAGACT CGAGGGGGGG CCCGGTACCT TTAAGACCAA TGACTTACAA			1880
GGCAGCTGTA GATCTTAGCC ACTTTTAAAGAAAAAGGGGG GGACTGGAAG GGCTAATTCA			1940
CTCCCAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC CACACACAAG GCTACTTCCC			2000
TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAAGATAT CCACTGACCT TTGGATGGTG			2060
CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAGAAGAG GCCAATAAAG GAGAGAACAC			2120
CAGCTTGTAA CACCCGTGTA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTAGA			2180
GTGGAGGTTT GACAGCCGCC TAGCATTCA TCACCTGGCC CGAGAGCTGC ATCCGGAGTA			2240
CTTCAGAACAC TGCTGACATC GAGCTTGCTA CAAGGGACTT TCCCCTGGGG ACTTTCCAGG			2300
GAGGCGTGGC CTGGGCGGGGA CTGGGGAGTG GCGAGCCCTC AGATGCTGCA TATAAGCAGC			2360
TGCTTTTGC CTGACTGGG TCTCTCTGGT TAGACCAAGAT CTGAGCCTGG GAGCTCTCTG			2420
GCTAACTAGG GAACCCACTG CTTAACGCTC AATAAAAGCTT GCCTTGAGTG CTTCAAGTAG			2480
TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG			2540
TGTGGAAAAT CTCTAGCACC CCCCAGGGAG TAGAGGTTGC AGTGAGCCAA GATCGCGCCA			2600
CTGCATTCCA GCCTGGCAA GAAAACAAGA CTGTCTAAA TAATAATAAT AAGTTAAGGG			2660
TATTAATAT ATTATACAT GGAGGTATA AAAATATATA TATTGGGCT GGGCGCAGTG			2720
GCTCACACCT GCGCCCCGGCC CTTGGGAGG CCGAGGCAGG TGGATCACCT GAGTTGGGA			2780
GTTCCAGACCC AGCCTGACCA ACATGGAGAA ACCCCTCTC TGTGTATTT TAGTAGATT			2840
TATTTATGT GTATTTTACAT CACAGGTATT TCTGGAAAAC TGAAACTGTT TTTCCTCTAC			2900
TCTGATACCA CAAGAACATCAGCACAGAG GAAGACTTCT GTGATCAAAT GTGGTGGAG			2960
AGGGAGGTTT TCACCAAGCAC ATGAGCAGTC AGTTCTGCCG CAGACTCGGC GGGTGTCCCT			3020
CGGTTCAAGTT CCAACACCGC CTGGCTGGAG AGAGGTCAAGA CCACAGGGTG AGGGCTCAGT			3080
CCCCAAGACA TAAACACCCA AGACATAAAC ACCAACAGG TCCACCCCGC CTGCTGCCCA			3140
GGCAGAGCCG ATTCAACCAAG ACAGGGATTA GGATAGAGAA AGAGTAAGTC ACACAGAGCC			3200
GGCTGTGCCG GAGAACGGAG TTCTTATTATG ACTCAAATCA GTCTCCCCAA GCATTCGGGG			3260
ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG TGAGTTGGAG ATGAAAGCGT			3320
AGGGAGTCGA AGGTGTCCTT TTGGCCCGAG TCAGTTCTG GGTGGGGGCC ACAAGATCGG			3380
ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT GGAGTGCAGG GTCTGAAAA			3440
TATCTCAAGC ACTGATTGAT CTTAGGTTT ACAATAGTGA TGTTACCCCA GGAACAATT			3500

GGGGAAGGTC AGAATCTTGT AGCCTGTAGC TGCATGACTC CTAACCATA ATTTCTTTT	3560
TGTTTTTTT TTTTATTT TGAGACAGGG TCTCACTCTG TCACCTAGGC TGGAGTGCAG	3620
TGGTGCAATC ACAGCTCACT GCAGCCCCA GAGCGGCCG CACCGCGGTG GAGCTCCAAT	3680
TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTG TTTTACAACG TCGTGAUTGG	3740
GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTT CGCCAGCTGG	3800
CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC	3860
GAATGGCGCG AAATTGTAAG CGTTAATATT TTGTTAAAAT TCCCGTTAAA TTTTGTAA	3920
ATCAGCTCAT TTTTAACCA ATAGGCCAA ATCGGCAAA TCCCTTATAA ATCAAAAGAA	3980
TAGACCGAGA TAGGGTTGAG TGTTGTTCCA GTTGGAAACA AGAGTCCACT ATAAAGAAC	4040
GTGGACTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG GCGATGGCCC ACTACGTGAA	4100
CCATCACCCCT AATCAAGTTT TTGGGGTGTG AGGTGCCGTG AAGCACTAAA TCGGAACCCCT	4160
AAAGGGAGCC CCCGATTAG AGCTTGACGG GGAAAGCCCG CGAACGTGGC GAGAAAGGAA	4220
GGGAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA GTGTAGCGGT CACGCTGCC	4280
GTAACCACCA CACCCGCCG CTTAATGCG CCGCTACAGG GCGCGTCCCA GGTGGCACTT	4340
TTGGGGAAA TGTGCGCGGA ACCCCTATTG GTTTATTTT CTAAATACAT TCAAATATGT	4400
ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCATAA ATATTGAAAA AGGAAGAGTA	4460
TGAGTATTCA ACATTTCCGT GTGCCCTTA TTCCCTTTTG TGCGGCATTT TGCTTCTG	4520
TTTTGCTCA CCCAGAAAG CTGGTGAAG TAAAAGATGC TGAAGATCAG TTGGGTGCA	4580
GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG	4640
AAGAACGTTT TCCAATGATG AGCACTTTA AAGTCTGCT ATGTGGCGCG GTATTATCCC	4700
GTATTGACGC CGGGCAAGAG CAACTCGGTC GCCGCATACTA CTATTCTCAG AATGACTTGG	4760
TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACCGATGG CATGACAGTA AGAGAATTAT	4820
GCAGTGCTGC CATAACCATG AGTGATAACA CTGGGCCAA CTTACTCTG ACAACGATCG	4880
GAGGACCGAA GGAGCTAACCG GCTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG	4940
ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAACGA CGAGCGTGAC ACCACGATGC	5000
CTGTAGCAAT GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT	5060
CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAAGT TGCGAGGACCA CTTCTGCC	5120
CGGCCCTTCC GGCTGGCTGG TTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC	5180
GCGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA	5240
CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT	5300
CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT	5360
TAAAATCTCA TTTTAATT AAAAGGATCT AGGTGAAGAT CCTTTTGAT AATCTCATGA	5420
CCAAAATCCC TTAACGTGAG TTTCGTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA	5480
AAGGATCTTC TTGAGATCCT TTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC	5540
CACCGCTACC AGCGGTGGTT TGTTGCGCG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG	5600
TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCT TCTAGTGTAG CCGTAGTTAG	5660

GCCACCACCTT CAAGAACCTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCCTGTTAC	5720
CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT	5780
TACCGGATAA GGCAGCAGCGG TCGGGCTGAA CGGGGGGTTG GTGCACACAG CCCAGCTTGG	5840
AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC	5900
TTCCCGAAGG GAGAAAGCGG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC	5960
GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTAA TAGTCCTGTC GGGTTTCGCC	6020
ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA	6080
ACGCCAGCAA CGCGGCCTTT TTACGGTTCC TGGCCTTTG CTGGCCTTT GCTCACATGT	6140
TCTTCTCTGC GTTATCCCT GATTCTGTGG ATAACCGTAT TACCCCTTT GAGTGAAGCTG	6200
ATACCGCTCG CGCGAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAAGCGAG GAAGCGGAAG	6260
AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCAATTAA TGCAAGCTGGC	6320
ACGACAGGTT TCCCAGCTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC	6380
TCACTCATTA GGCACCCAG GCTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA	6440
TTGTGAGCGG ATAACAATT CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG	6500
GAATTAACCC TCACTAAAGG GAACAAAAGC TGCTGCAGGG TCCCTAACTG CCAAGCCCCA	6560
CAGTGTGCC CGAGGCTGCC CCTTCCTCT AGCGGCTGCC CCCACTCGGC TTTGCTTCC	6620
CTAGTTTCAG TTACTTGCAGT TCAGCCAAGG TCTGAAACTA GGTGCGCACA GAGCGGTAAG	6680
ACTGCGAGAG AAAGAGACCA GCTTACAGG GGGTTATCA CAGTGCACCC TGACAGTCGT	6740
CAGCCTCACA GGGGGTTAT CACATTGCAC CCTGACAGTC GTCAAGCTCA CAGGGGGTTT	6800
ATCACAGTGC ACCCTTACAA TCATTCCATT TGATTCAAA TTTTTTAGT CTCTACTGTG	6860
CCTAACTTGT AAGTTAAATT TGATCAGAGG TGTGTTCCA GAGGGGAAAA CAGTATATAAC	6920
AGGGTTCACT ACTATCGCAT TTCAGGCCTC CACCTGGGTC TTGGAATGTG TCCCCCGAGG	6980
GGTGATGACT ACCTCAGTTG GATCTCCACA GGTACAGTG ACACAAGATA ACCAAGACAC	7040
CTCCCAAGGC TACCAACATG GGCCCCCTC CACGTGCACA TGGCCGGAGG AACTGCCATG	7100
TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTGGTG TGGAGGGAGG GACCAGCGCA	7160
GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG CCCAGTTCT ACTTACACCA	7220
GGAAAGGC	7228

(131) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) TOPOLOGY: LINEAR
- (ii) MOLECULAR TYPE: PROTEIN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Tyr Lys Leu Lys
20 25 30
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110
Lys Lys Ala Gln Gln Ala Ala Asp Thr Gly His Ser Asn Gln Val
115 120 125
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195 200 205
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
210 215 220
Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
225 230 235 240
Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
245 250 255
Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
260 265 270
Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
275 280 285
Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
290 295 300
Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
305 310 315 320
Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
325 330 335
Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
340 345 350
Val Gly Gly Pro Gly His Lys Ala Arg Val Leu
355 360